

Figure 1

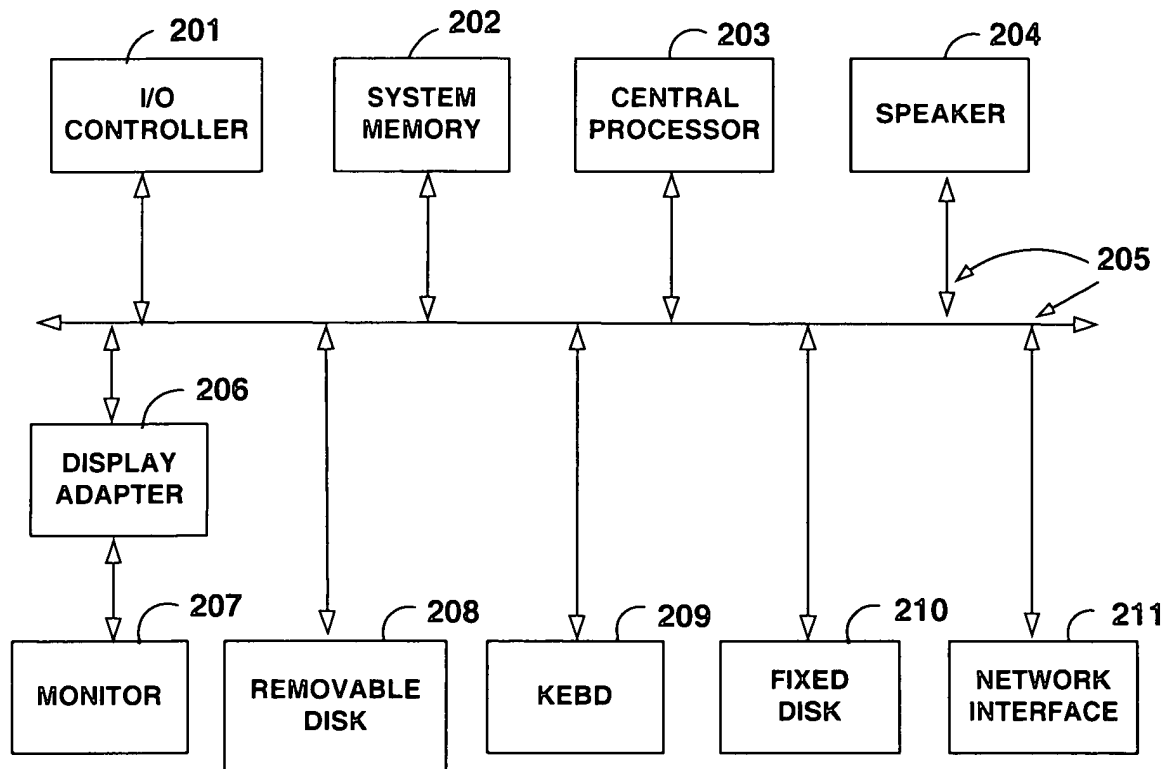
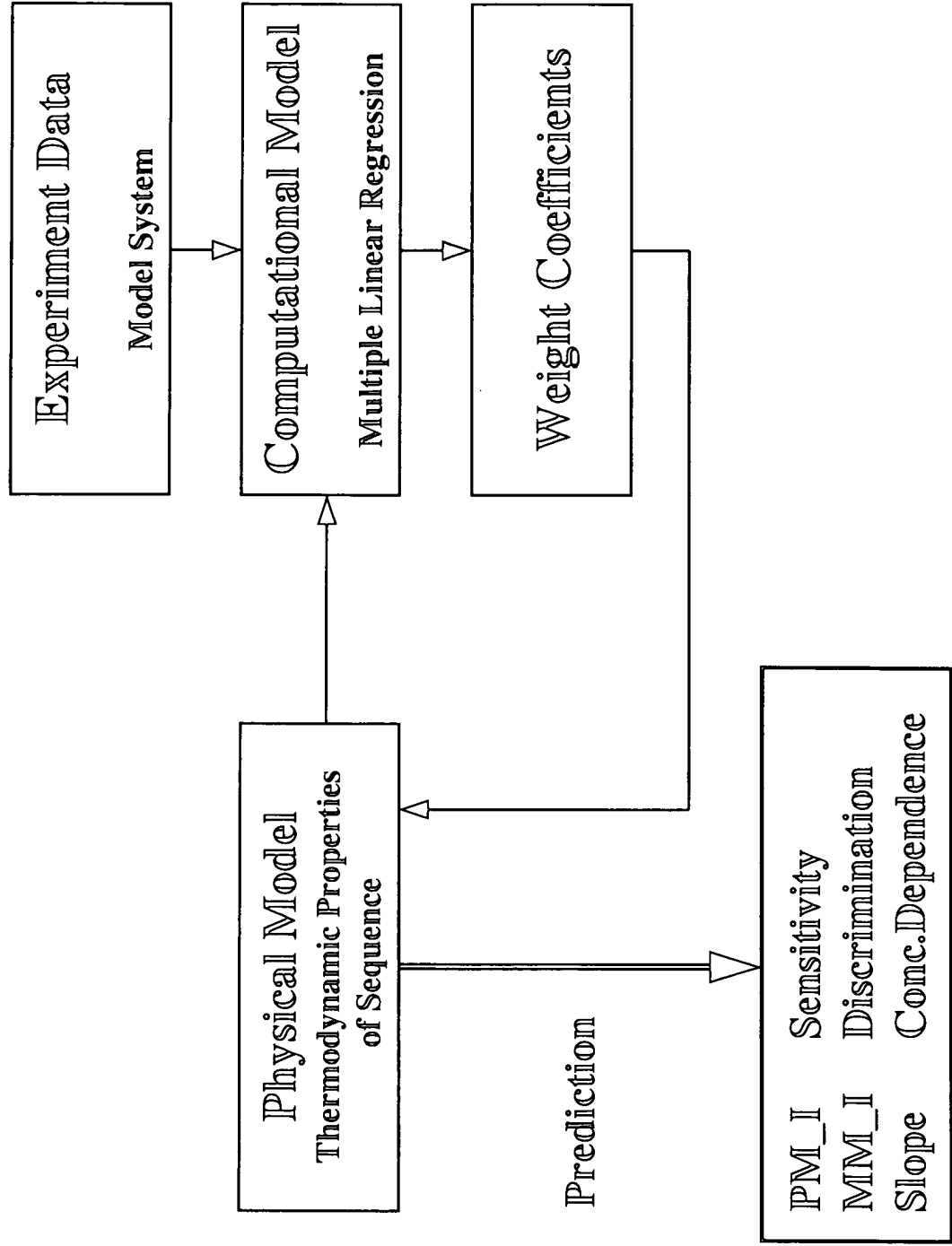


Figure 2

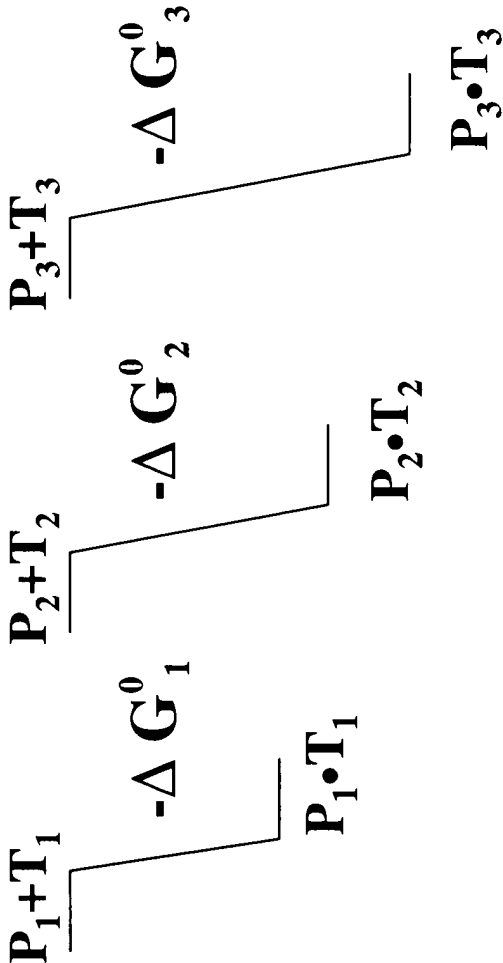
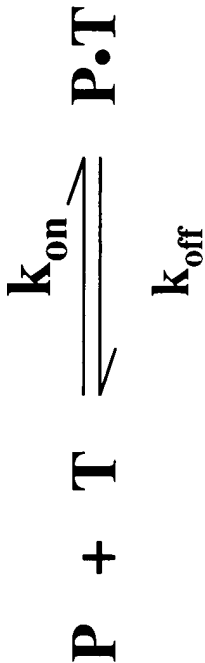
001221" 59654260
Predicting Probe Quality

Figure 3



Basic Physical Model

Figure 4



Define Each Nucleotide at Each position

Figure 5

Example : GTCA

*Using A as ref. 3 base/position

i	<u>Position</u>	<u>Base</u>	<u>S_i</u>
1	1	C	0
2	1	G	1
3	1	T	0
(1 st position is G)			
4	2	C	0
5	2	G	0
6	2	T	1
(2 nd position is T)			
7	3	C	1
8	3	G	0
9	3	T	0
(3 rd position is C)			
10	4	C	0
11	4	G	0
12	4	T	0
(4 th position is A as reference)			



Relative ΔG vs. Base Position

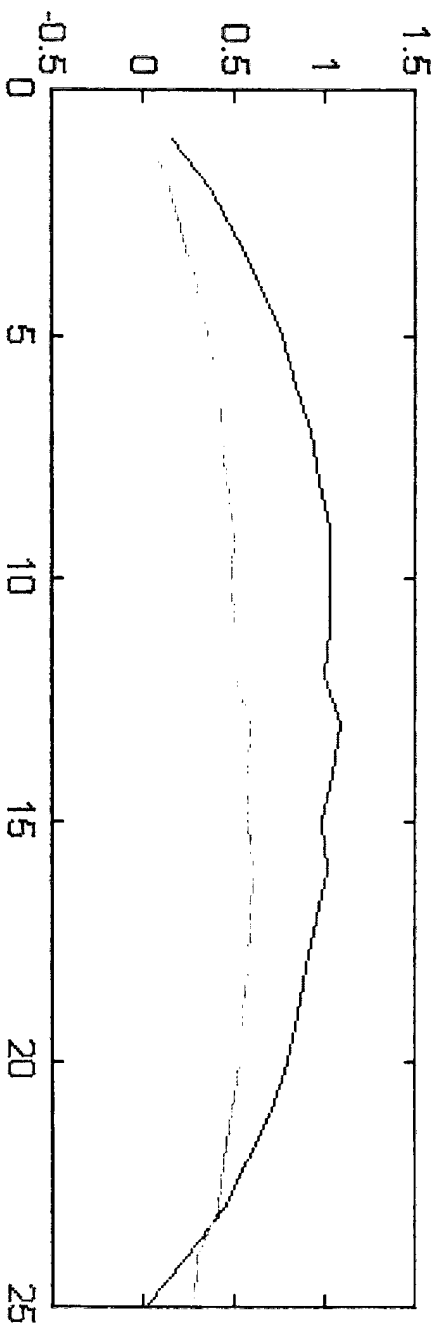


Figure 6A

PM

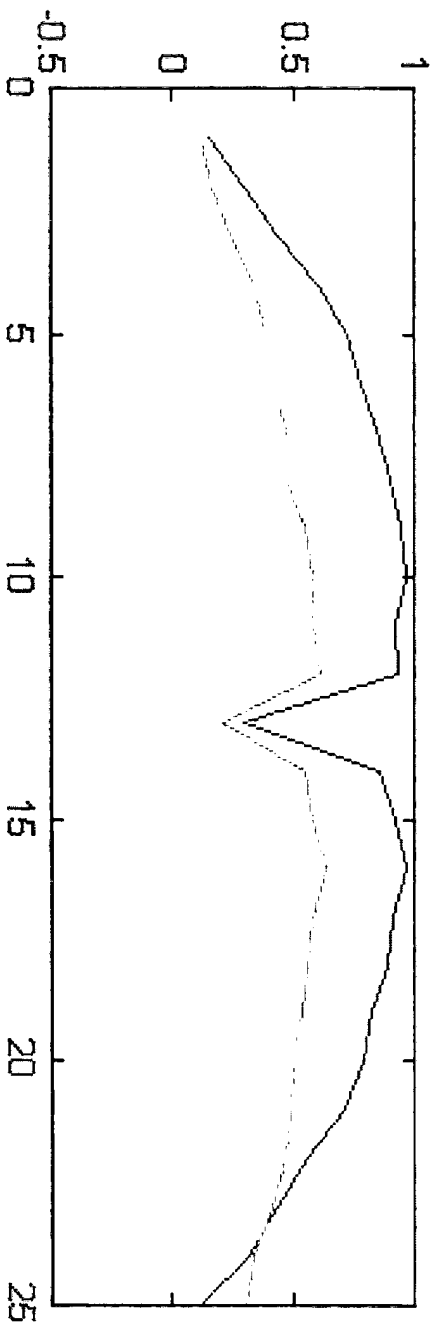


Figure 6B

MM

Base Position in Probe Sequence

US 2005/0166113 A1

Overall Reaction

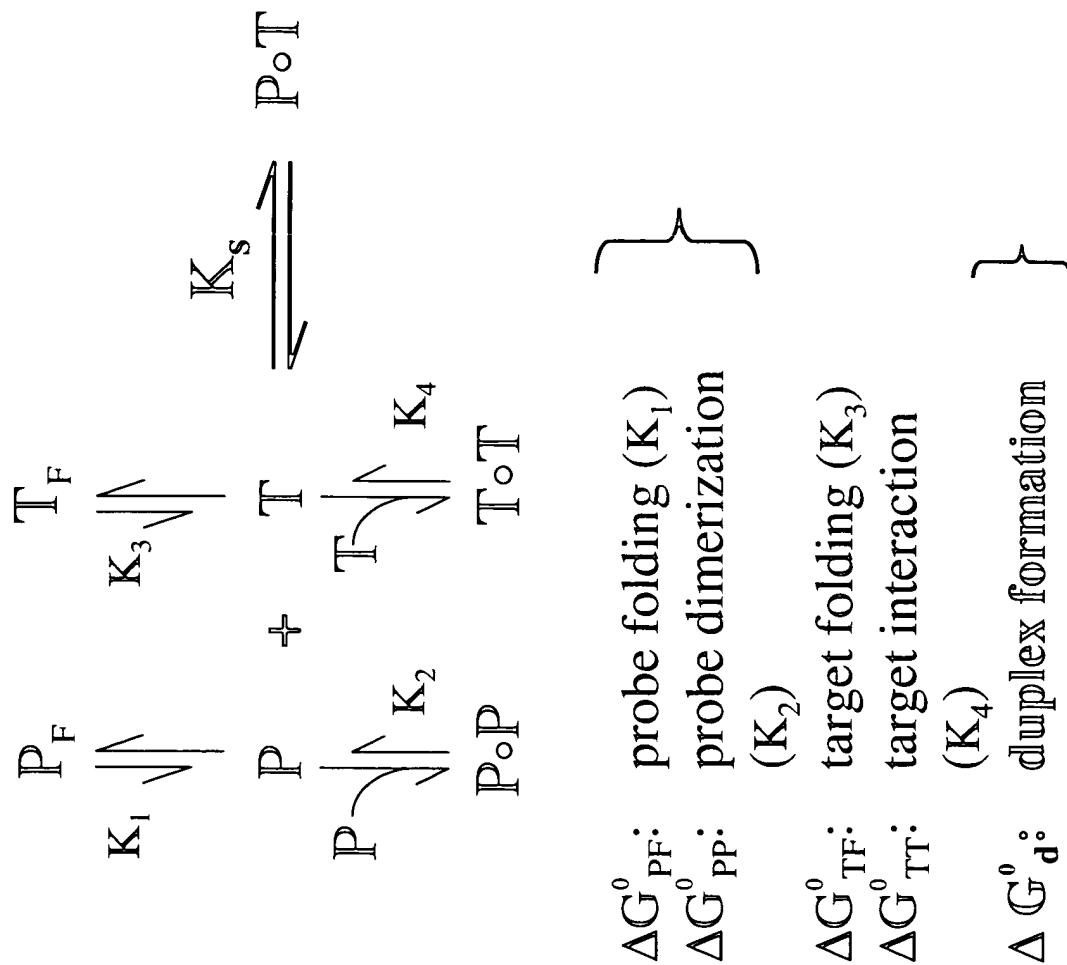


Figure 7



Concentration Dependence: Slope

Figure 8

$$\ln I = S \cdot \ln C + \ln K_{app}$$

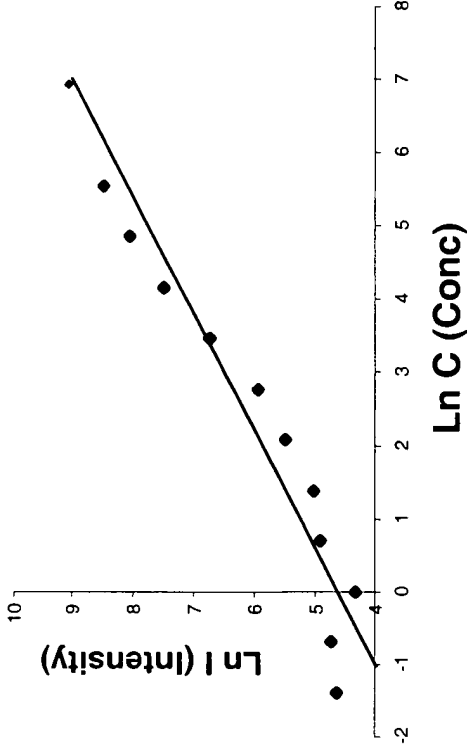
$$I = K_{app} \cdot C^S$$

I: Intensity

K_{app}: Apparent Affinity Constant

C: Concentration

S: Empirical Value (0 < S < 1)



Relationship between Kapp vs. S

- Prediction of Probe Saturation

Figure 9A

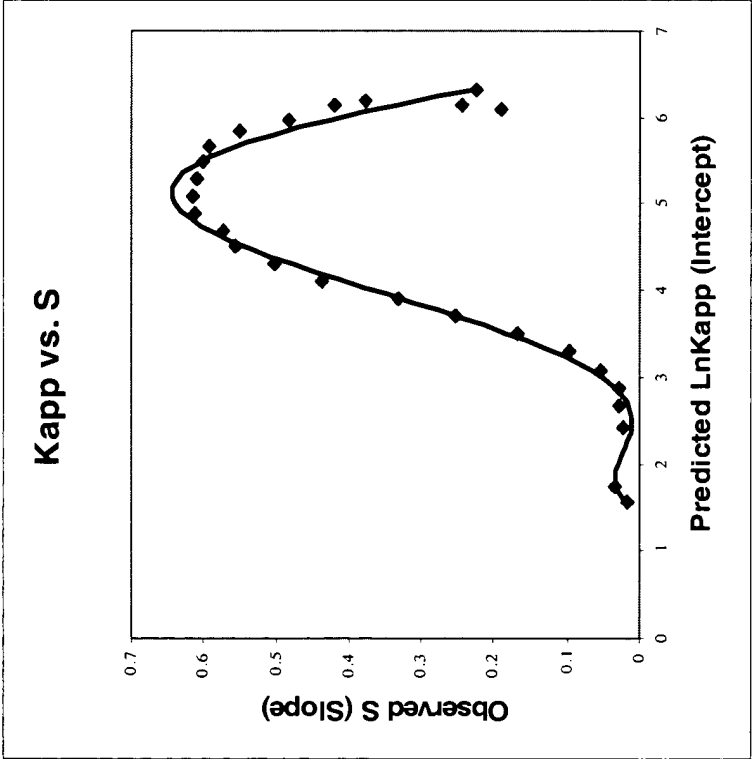
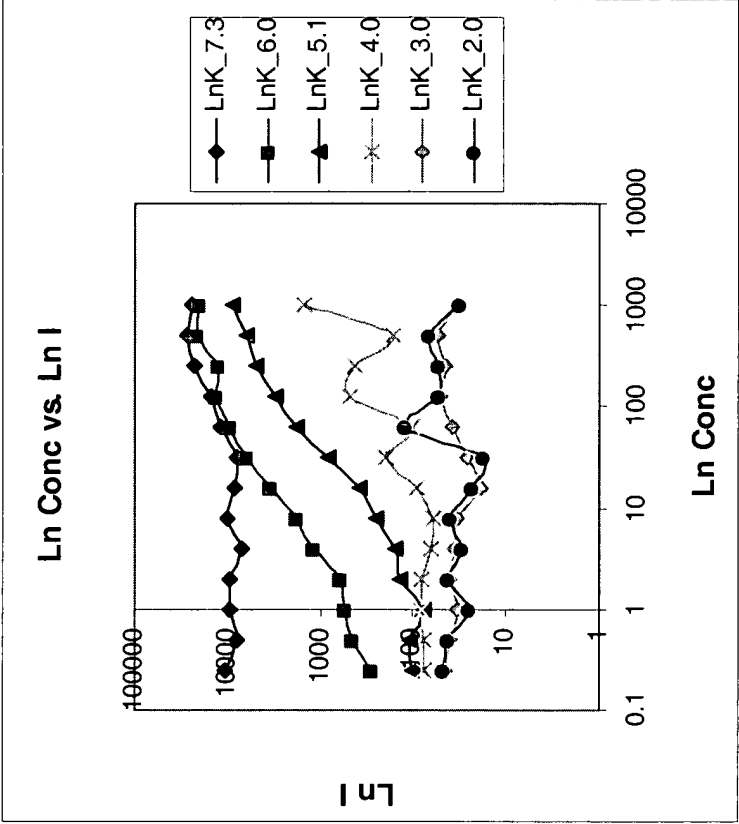


Figure 9B



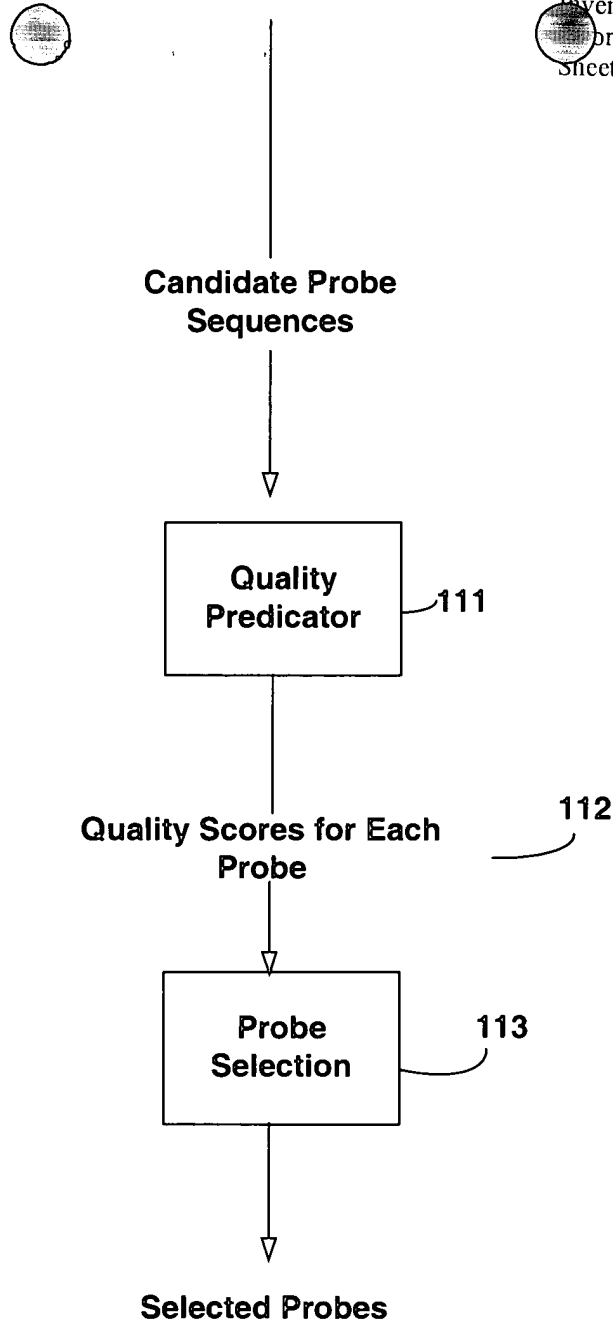


Figure 10

09745965-122100 DOT27-59634260

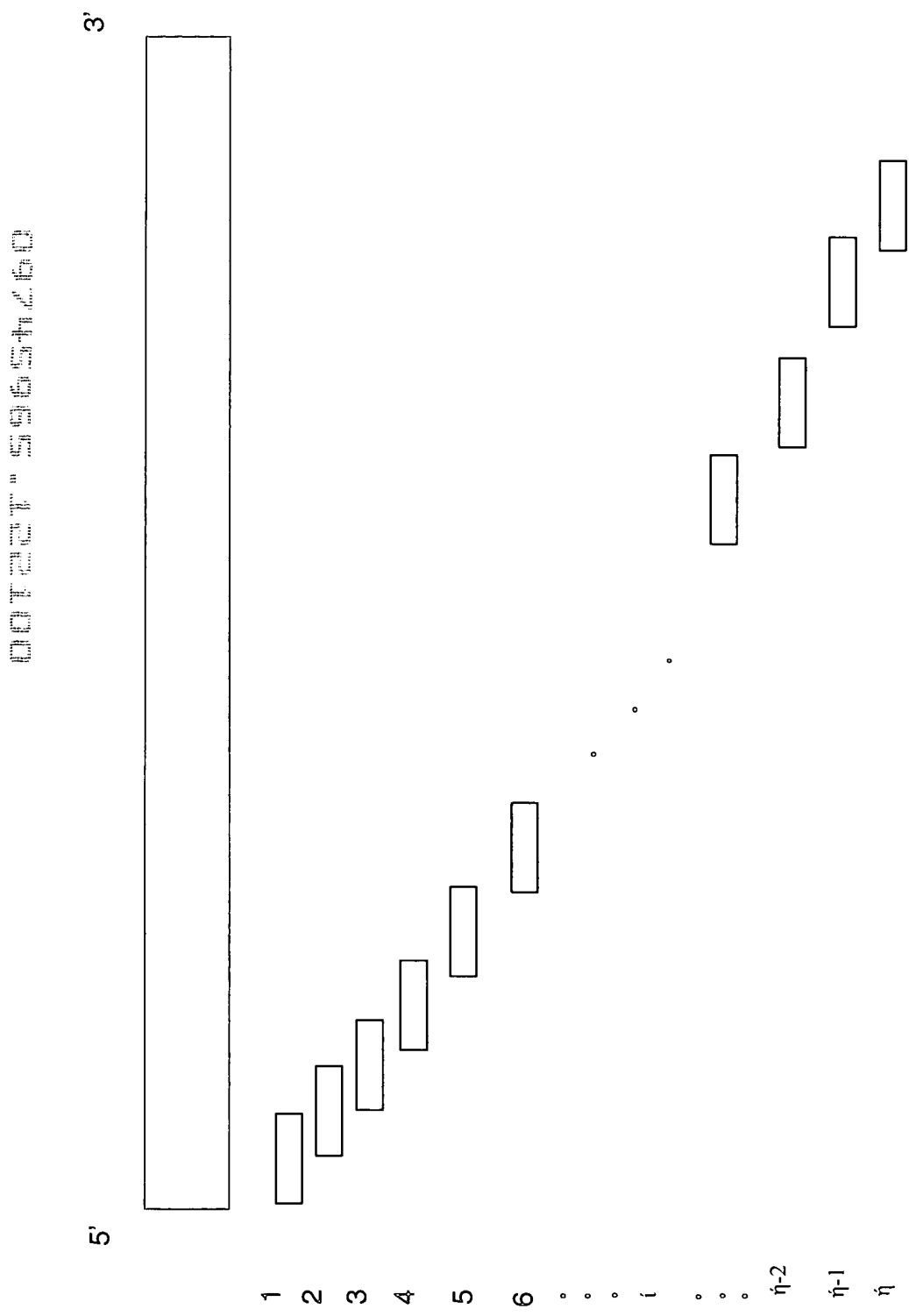


FIGURE 11

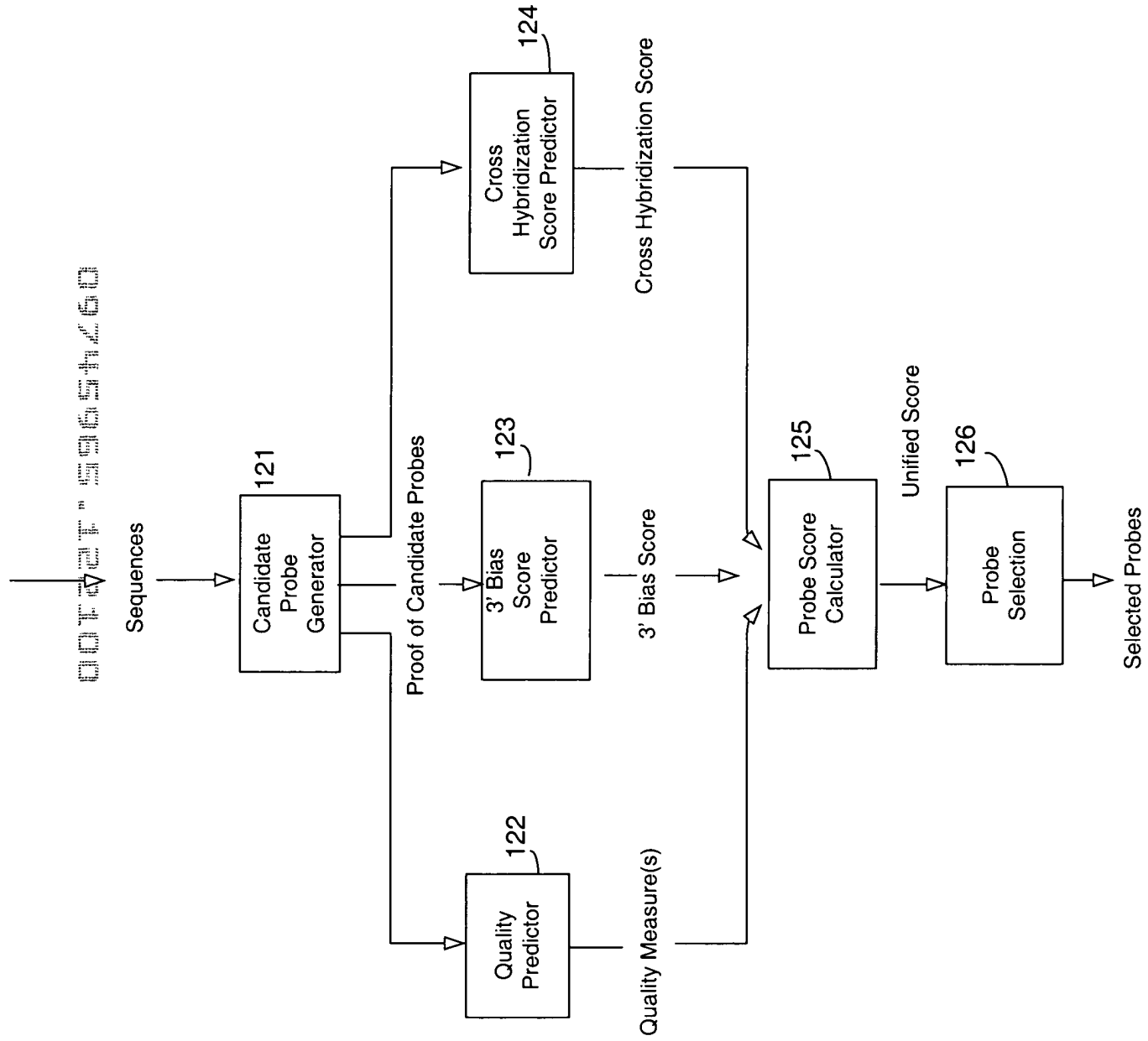


Figure 12

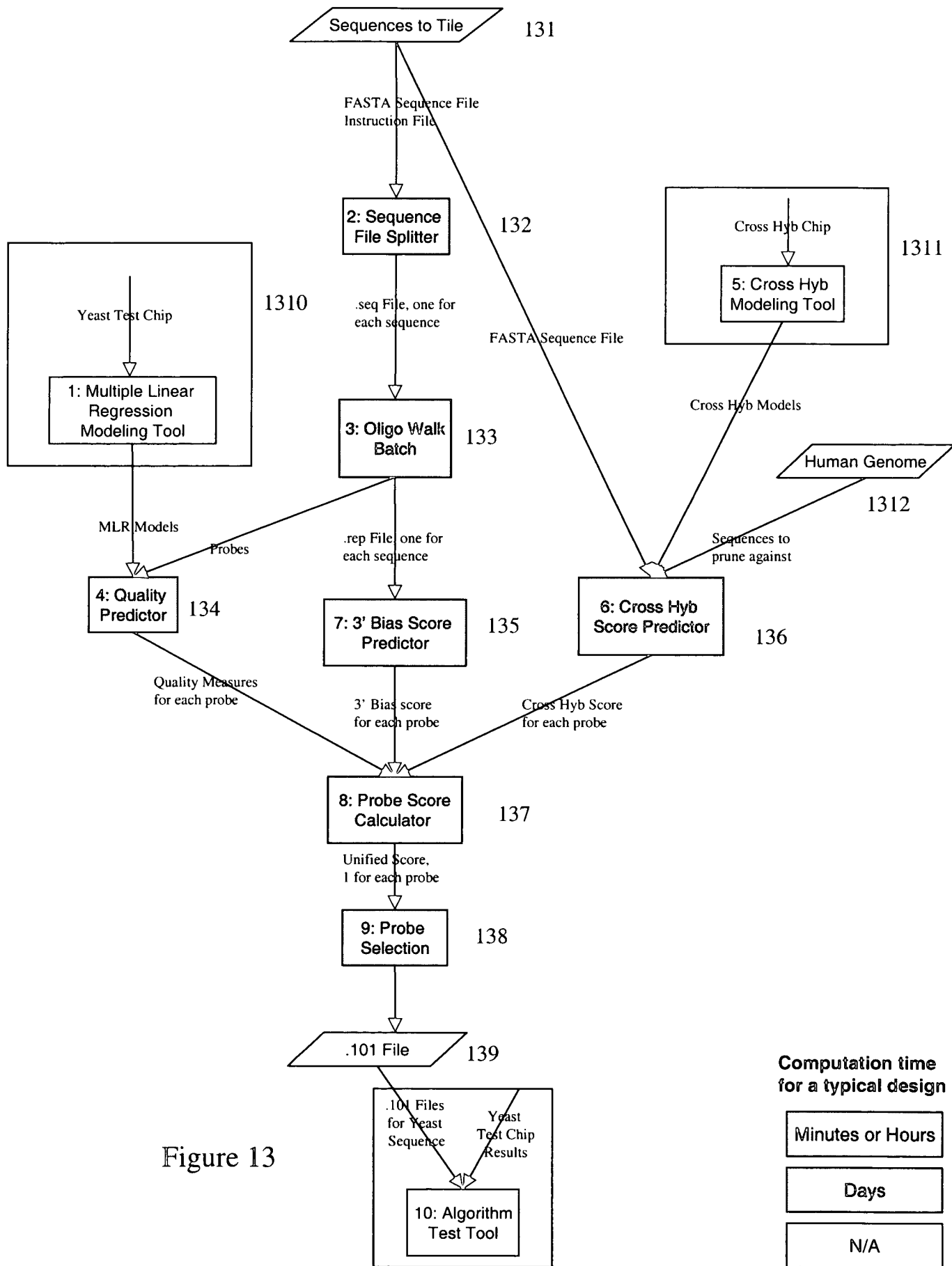


Figure 13

Computation time
for a typical design

Minutes or Hours
Days
N/A

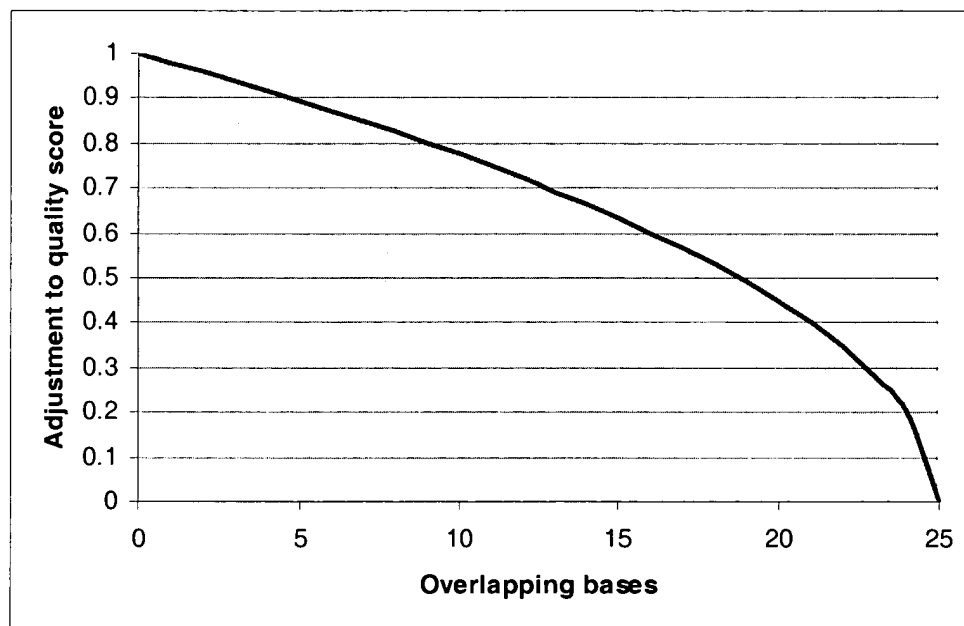
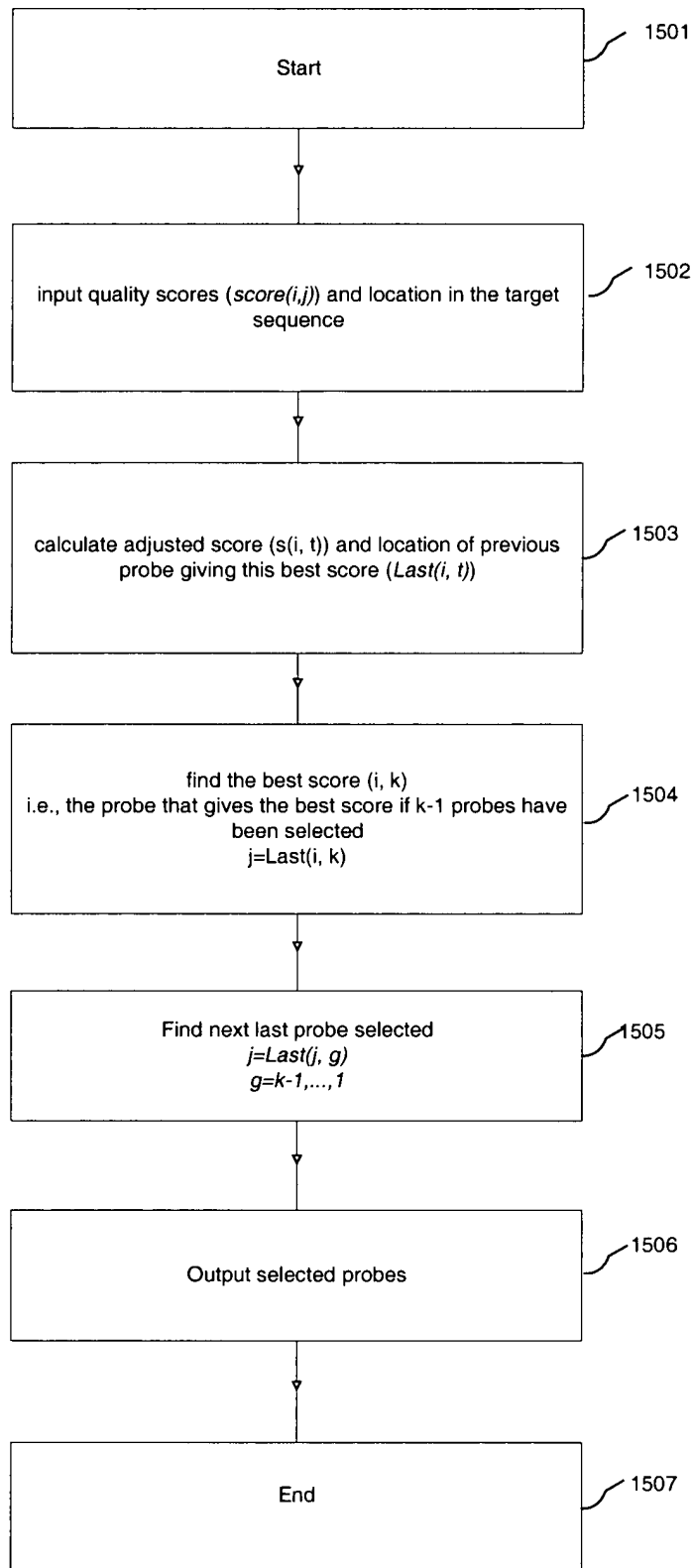


Figure 14



Latin Square MLR

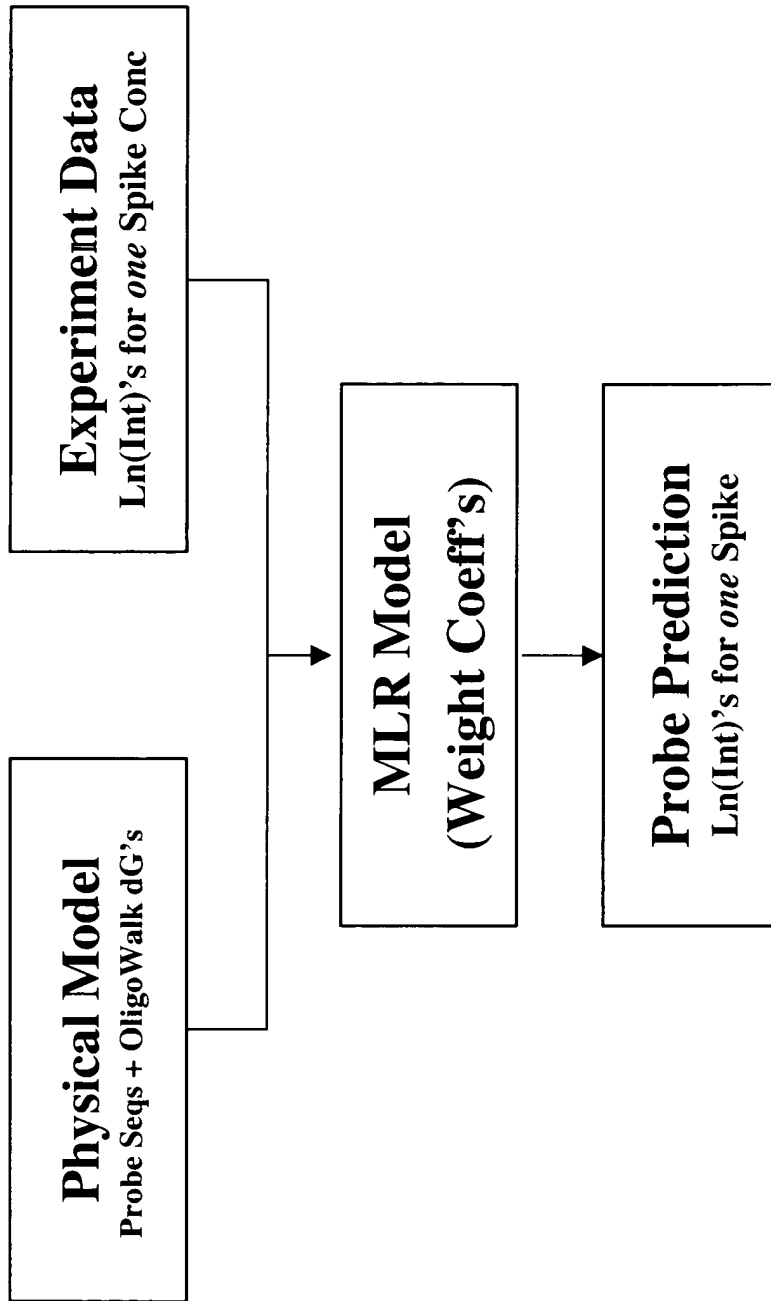


Figure 16

112 Yeast Clones Randomly Divided into 14 Groups

Groups

1	2	3	4	5	6	7	8	9	10	11	12	13	14
YNL259C	YNL037C	YAL038W	YHR044C	YMR127C	YLR377C	YOL064C	YPL209C	YIR034C	YJR148W	YEL046C	YGR185C	YBR166C	YOL165C
YEL003W	YDR113C	YLR083C	YJL117W	YNL290W	YOL086C	YJR094C	YFL029C	YMR276W	YML060W	YGR072W	YGL181W	YJL155C	YNL227C
YDL235C	YGL105W	YLL043W	YMR116C	YMR228W	YJR019C	YIR026C	YGR040W	YMR294W	YDL188C	YMR203W	YGL213C	YEL036C	YNL228W
YEL024W	YDR498C	YBR212W	YPL111W	YPR057W	YOR085W	YLR056W	YPR065W	YPL001W	YGR109C	YGR112W	YOL136C	YJL014W	YMR108W
YEL018W	YDL029W	YNL015W	YCL055W	YNR035C	YDL226C	YMR270C	YPR191W	YFL039C	YOL043C	YHR208W	YEL037C	YJL110C	YPL043W
YER161C	YKL081W	YDL075W	YFR025C	YCL032W	YBL016W	YBR018C	YMR139W	YNL307C	YLR291C	YIL136W	YHL022C	YFL056C	YLR153C
YKL193C	YFR053C	YML098W	YLR354C	YIL154C	YBL068W	YBR057C	YPR035W	YGL148W	YDR088C	YOR099W	YHL014C	YJR155W	YPR074C
YPR129W	YFL018C	YOL143C	YPL069C	YBR034C	YHR025W	YER118C	YNL005C	YGL155W	YMR015W	YOR176W	YKR061W	YNL331C	YPL089C

Figure 17

Latin Square Experiment

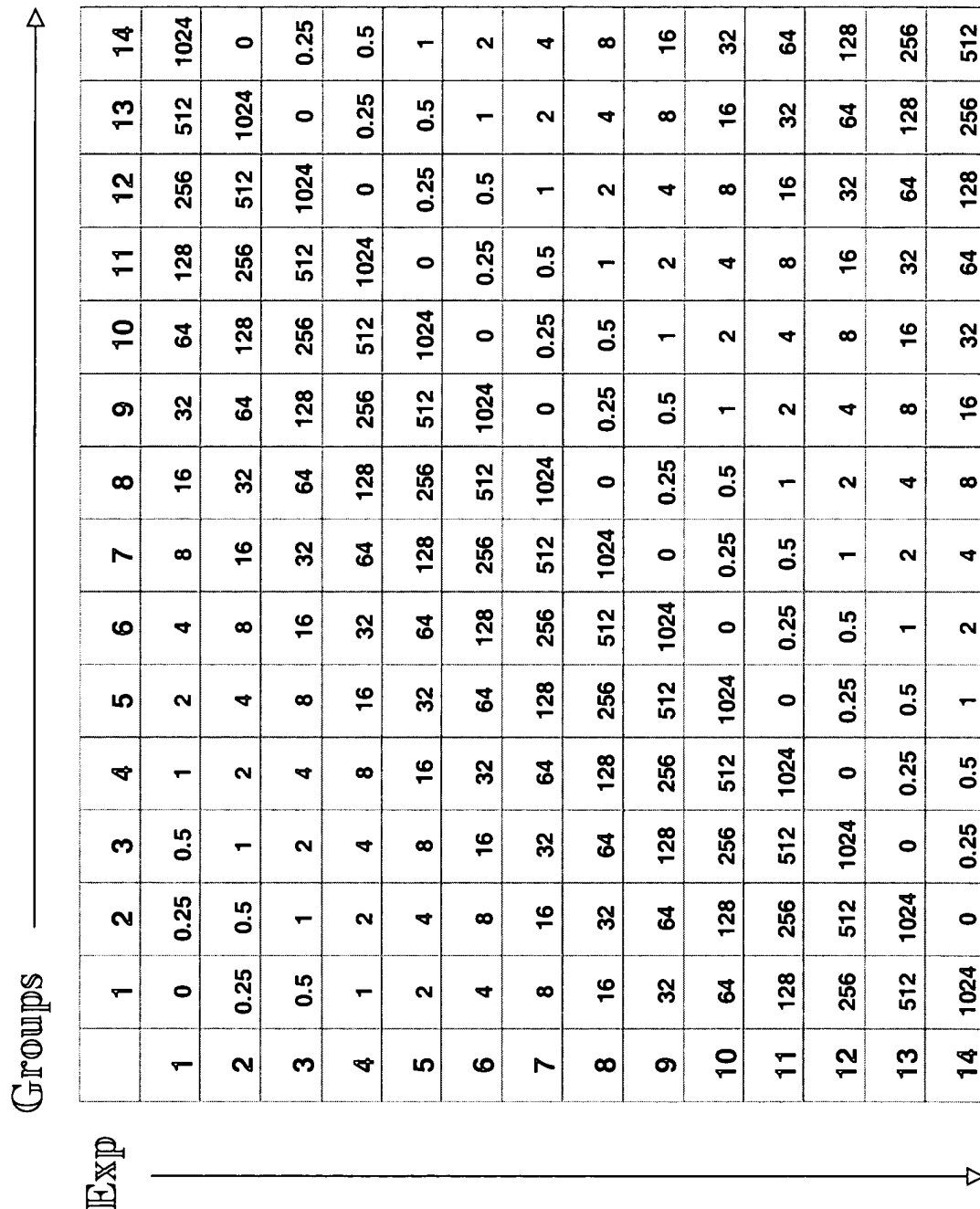


Figure 18

Latin Square Data Sets from Yeast_Test_Hlyb Chips

<i>Lot 1 (9912072)</i>			
No Background:	3 Scans	14 chips	(530, PMT=701; 570, PMT=701; 570, PMT=600)
+ Background:	3 Scans	14 chips	(530, PMT=701; 570, PMT=701; 570, PMT=600)
<i>Lot 2 (9910426)</i>			
No Background:	1 Scan	14 chips	(570, PMT=600)
No Background:	1 Scan	14 chips	(570, PMT=600)
<i>Lot 3 (9910427)</i>			
+ Background:	1 Scan	14 chips	(570, PMT=526)
No Background_Rep1:	1 Scan	14 chips	(570, PMT=526)
No Background_Rep2:	1 Scan	14 chips	(570, PMT=526)
<i>Lot 4 (9913514)</i>			
No Background:	1 Scan	14 chips	(570, PMT=526)
+ Background:	1 Scan	14 chips	(570, PMT=526)
<i>Lot 5 (9914059)</i>			
+ Background_Rep1:	1 Scan	14 chips	(570, PMT=526)
+ Background_Rep2:	1 Scan	14 chips	(570, PMT=526)
No Background:	1 Scan	14 chips	(570, PMT=526)

Figure 19

Bootstrapping

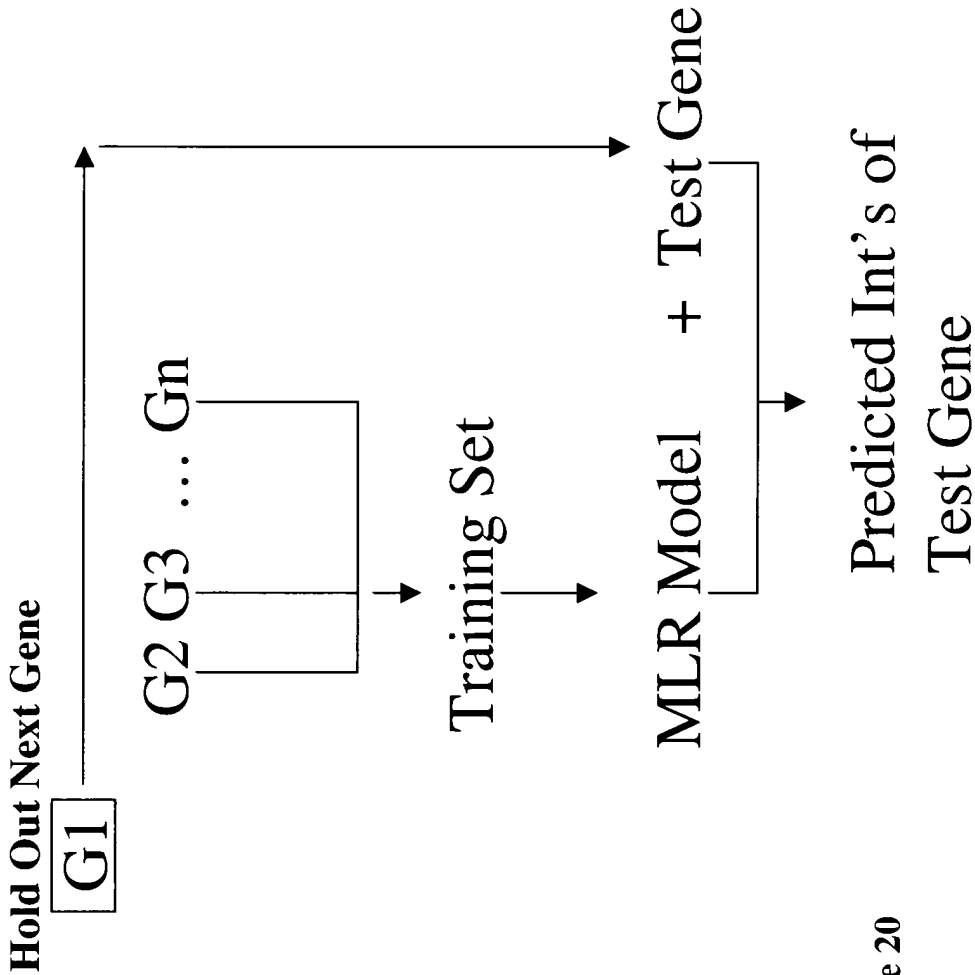


Figure 20



YDR113C
Figure 21A

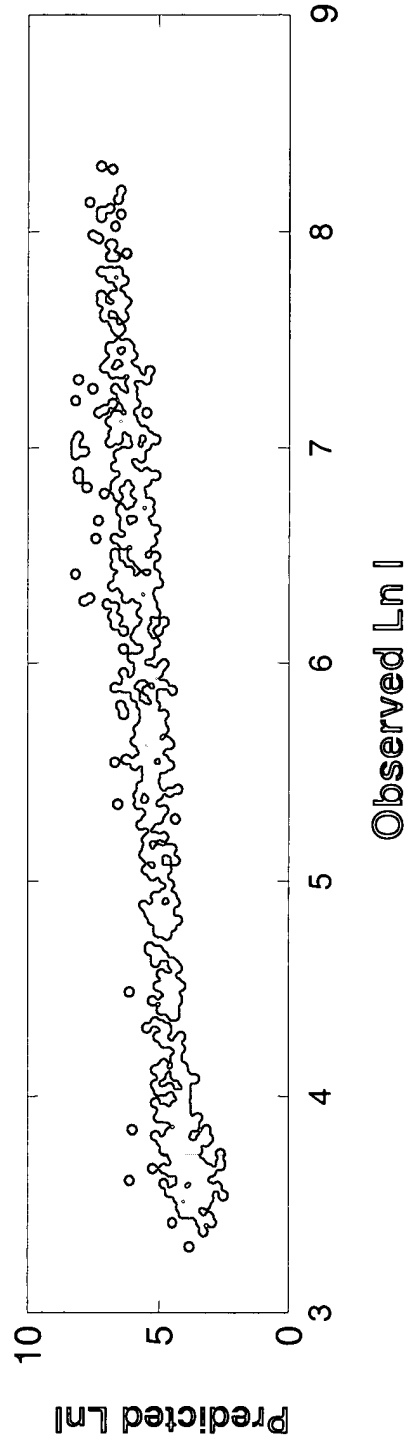
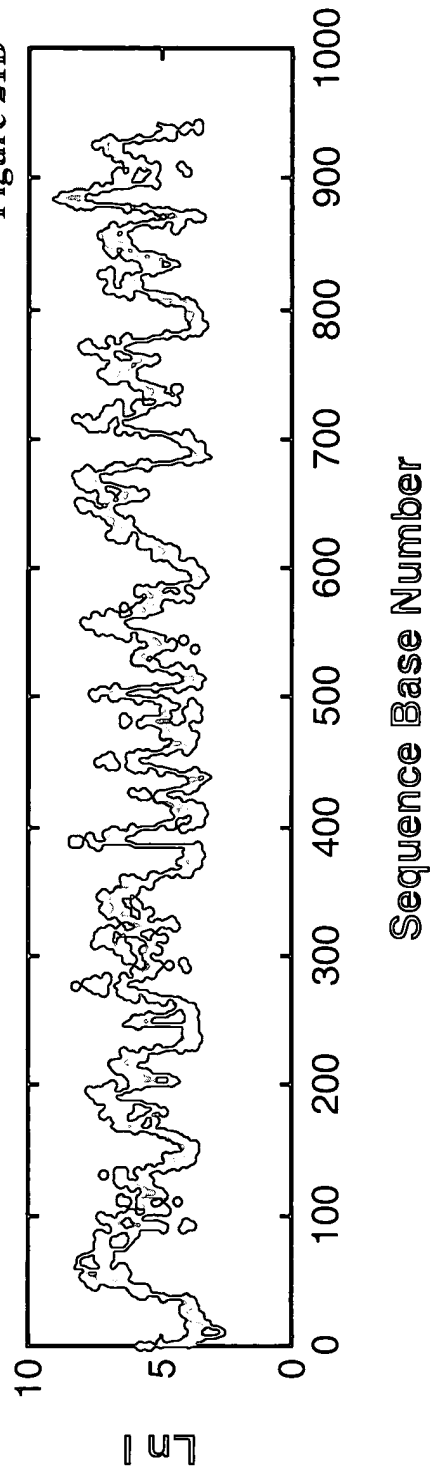


Figure 21B



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YGR109C

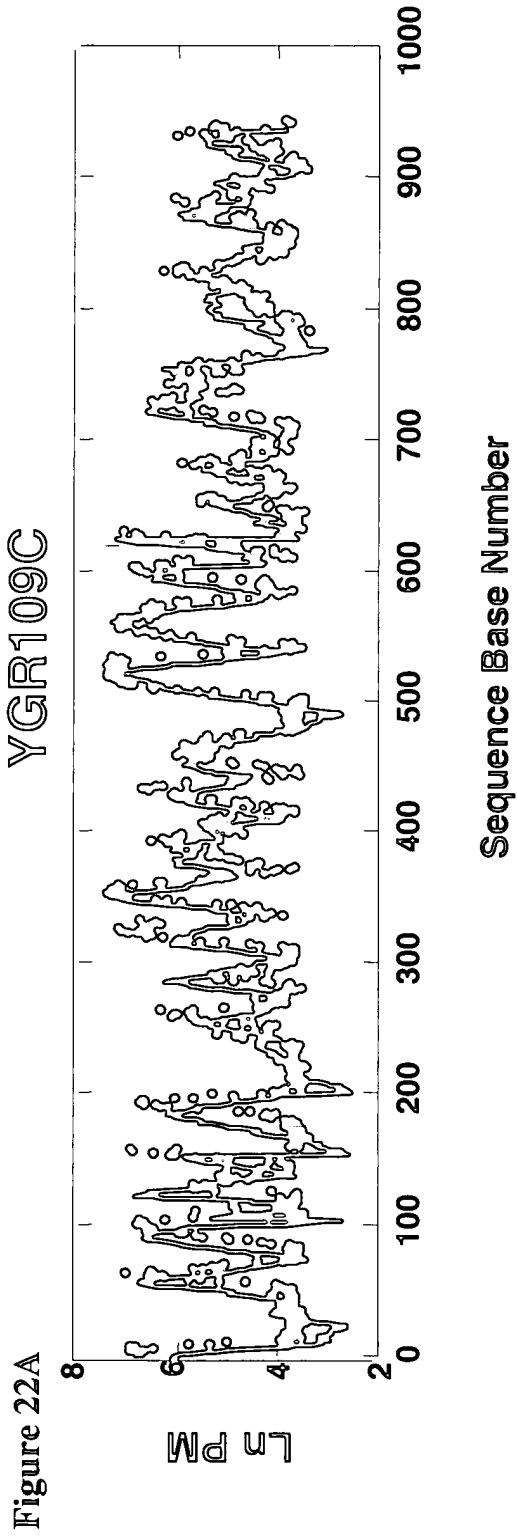
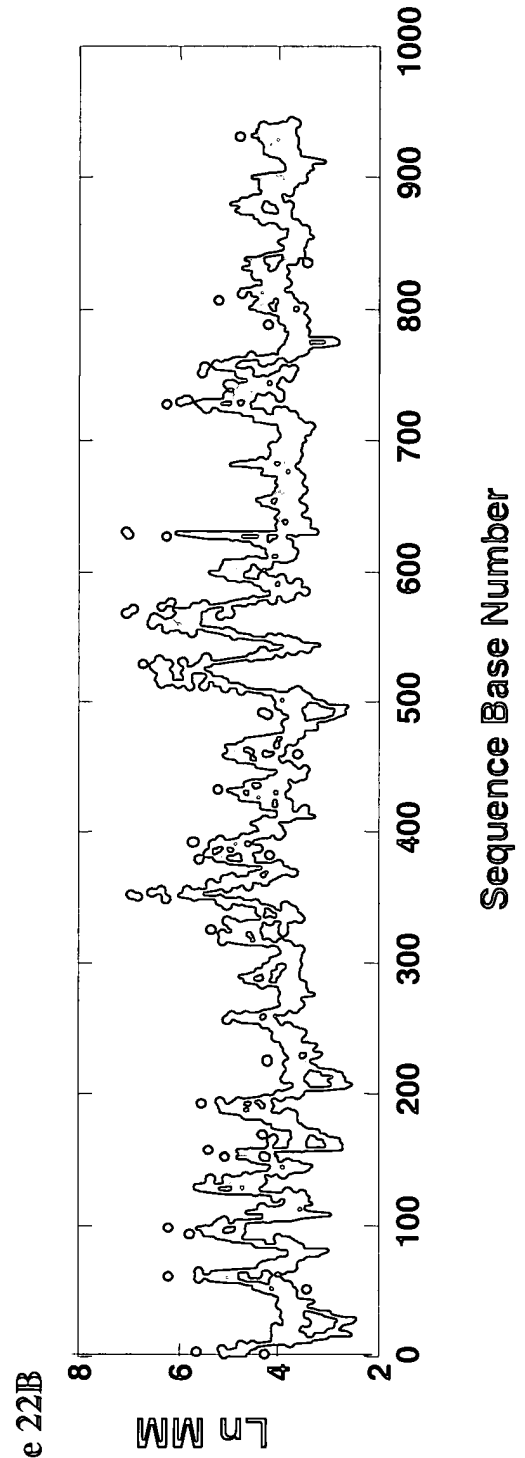


Figure 22B



Ln(Int) at Different Spike Concentrations

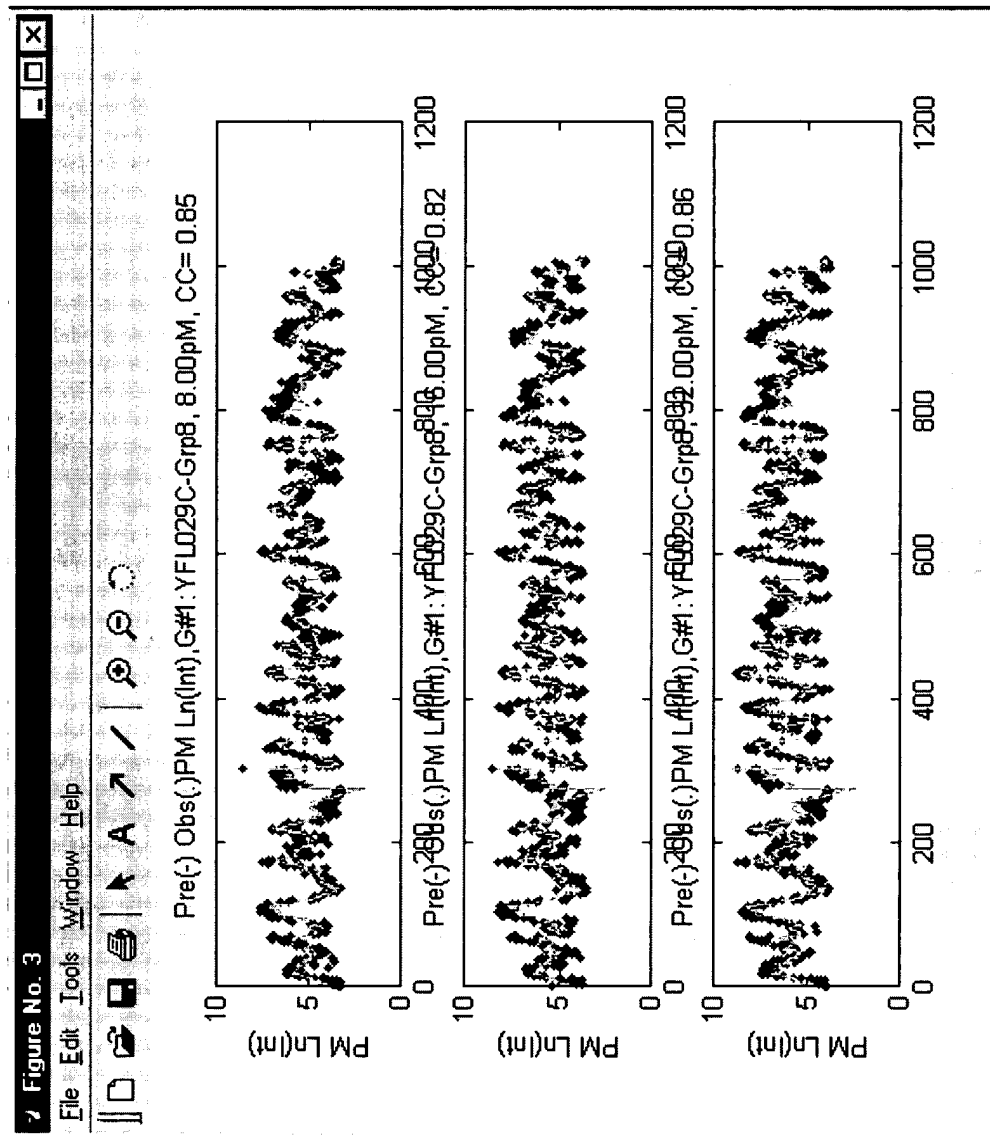


Figure 23

Correlation between Predicted & Observed $\text{Ln}(\text{Int})$'s

Title: Methods for Selecting Nucleic Acid Probes
Inventor: Hubbell
Attorney Docket No. 3373.1
Sheet 24 of 30

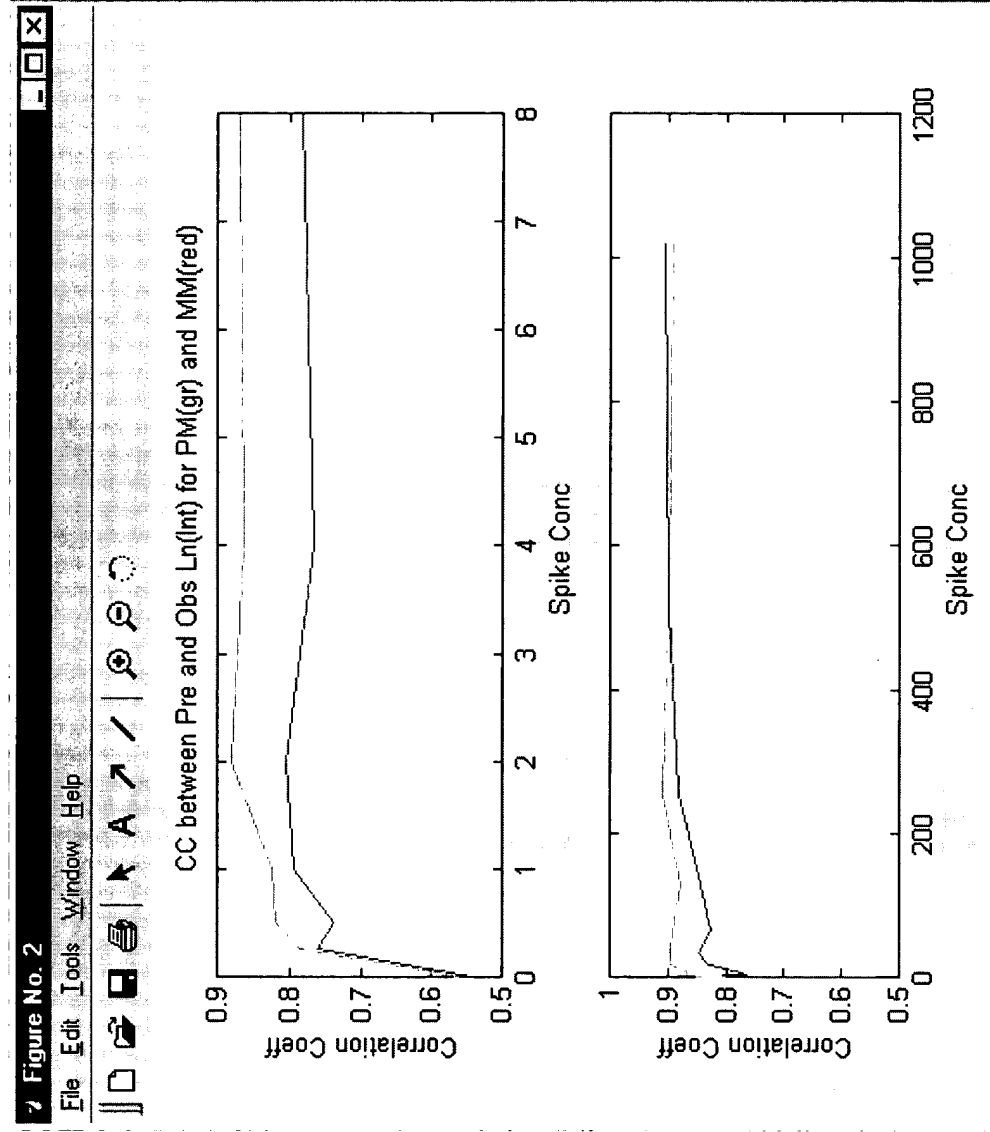


Figure 24

Negative Control: Gene in Wrong Orientation

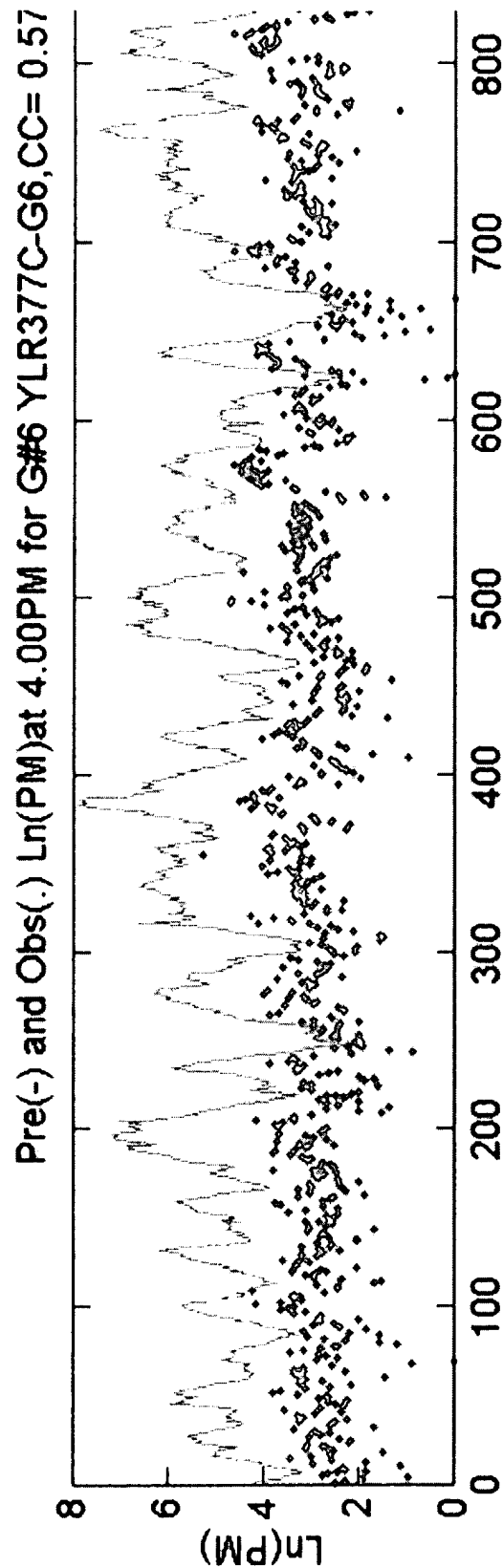


Figure 25

Predicted Observed Slopes

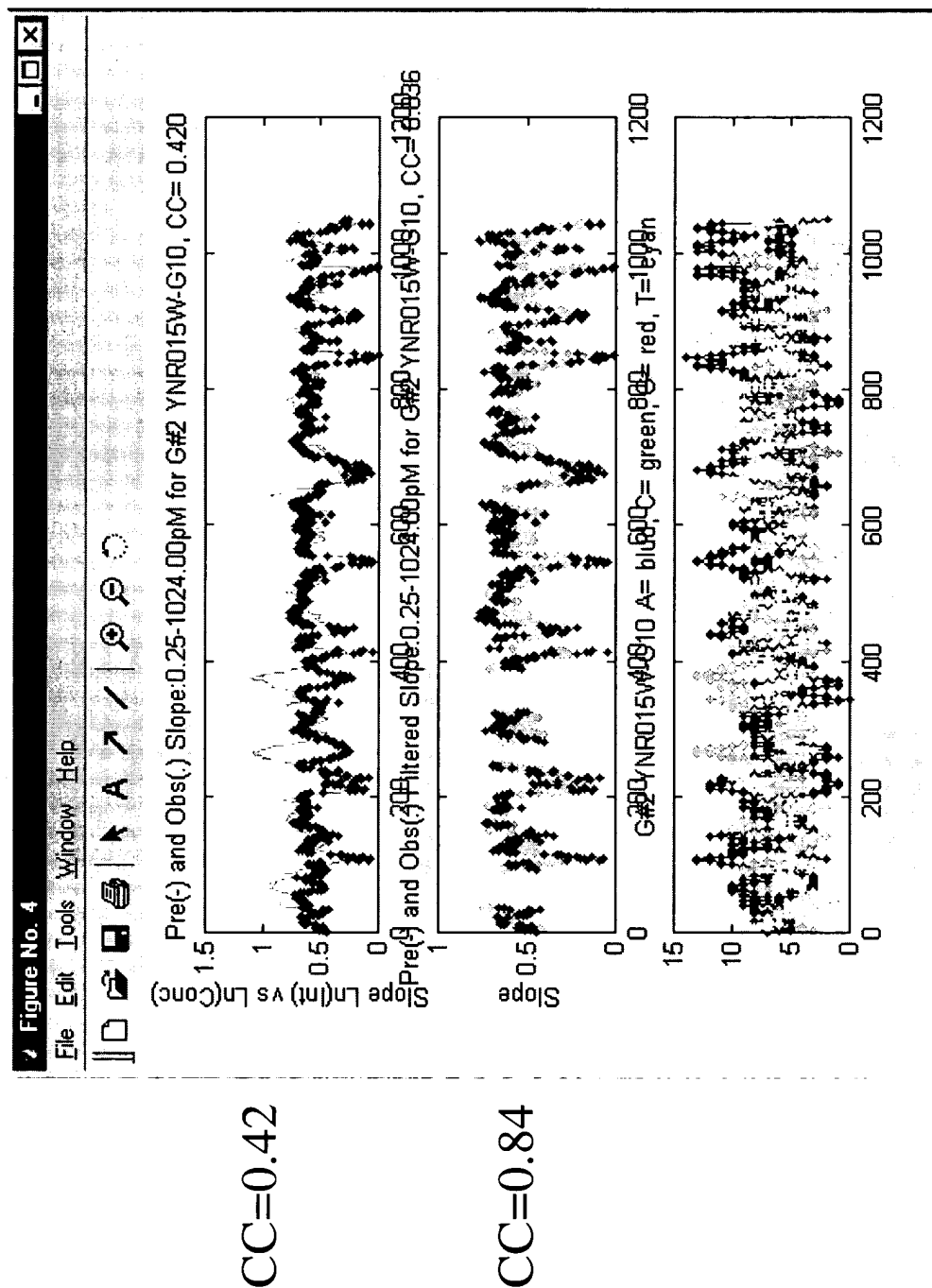
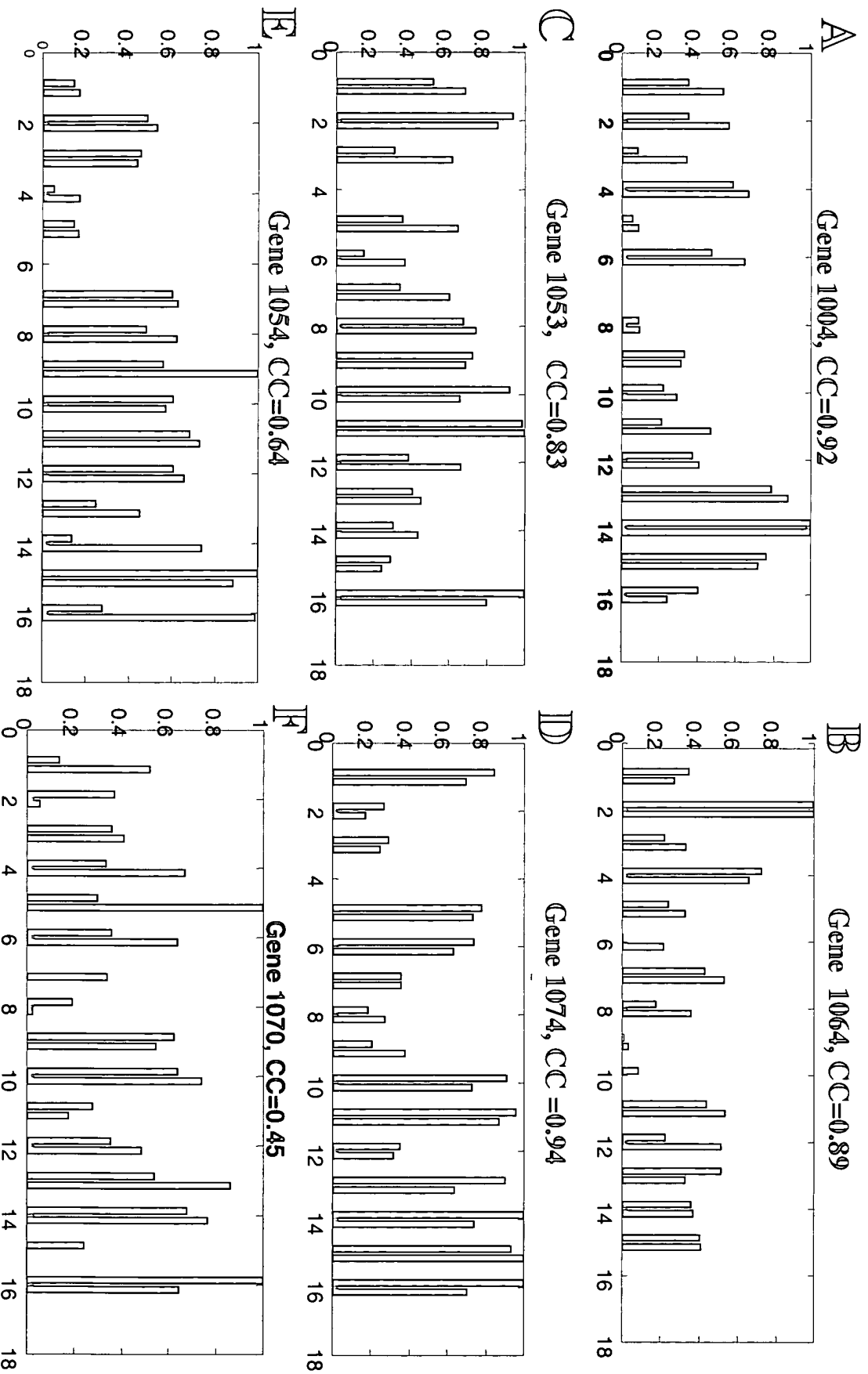


Figure 26

From Yeast to Human

Figure 27

Using Parameters from Yeast Model System to Predict Human U95A



001221" 59554260

Predictions for Hu_U95a Probe Sets

Title: Methods for Selecting Nucleic Acid
Probes
Inventor: Hubbell
Attorney Docket No. 3373.1
Sheet 28 of 30

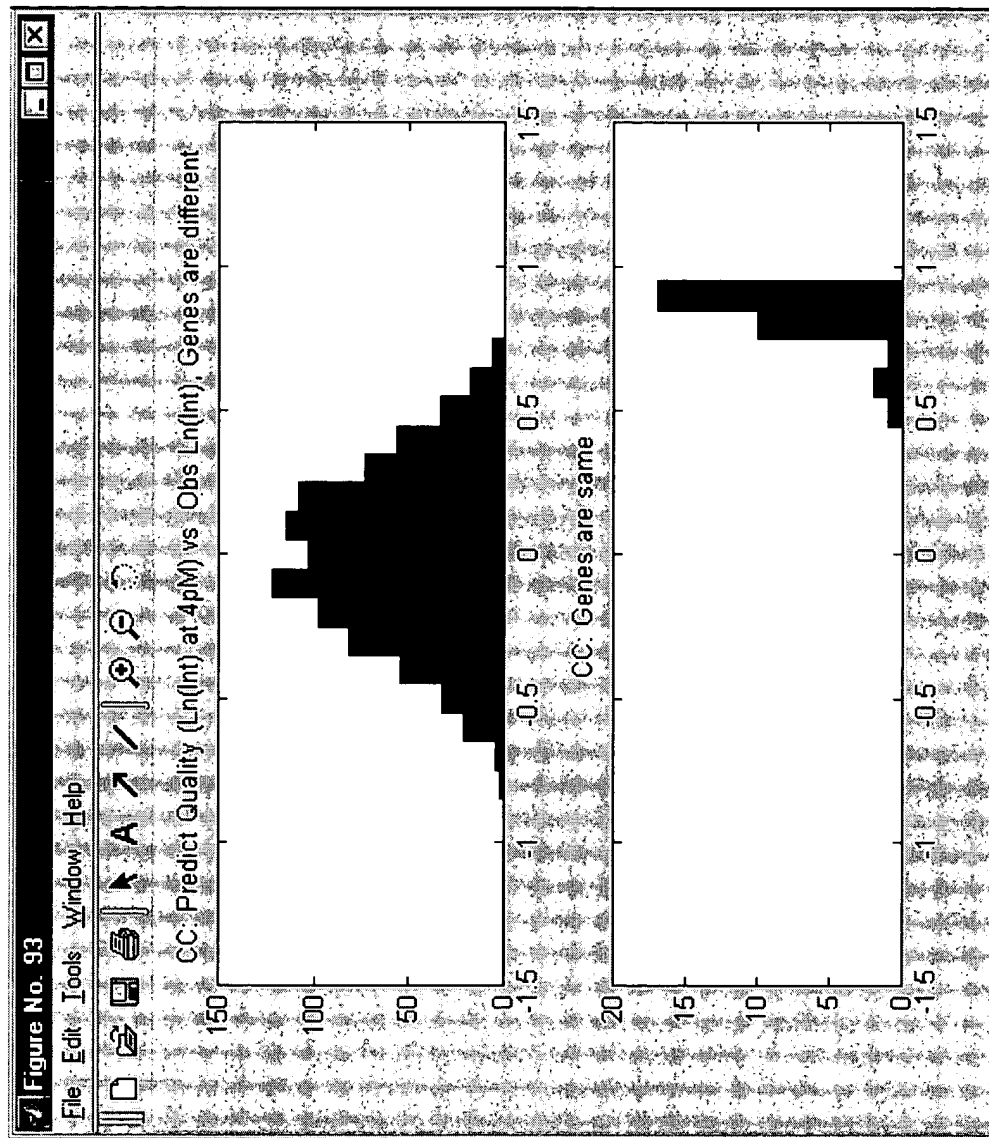


Figure 28

DOT22T" 59654260

Sixteen Probes Selected By Dynamic Programming Algorithm

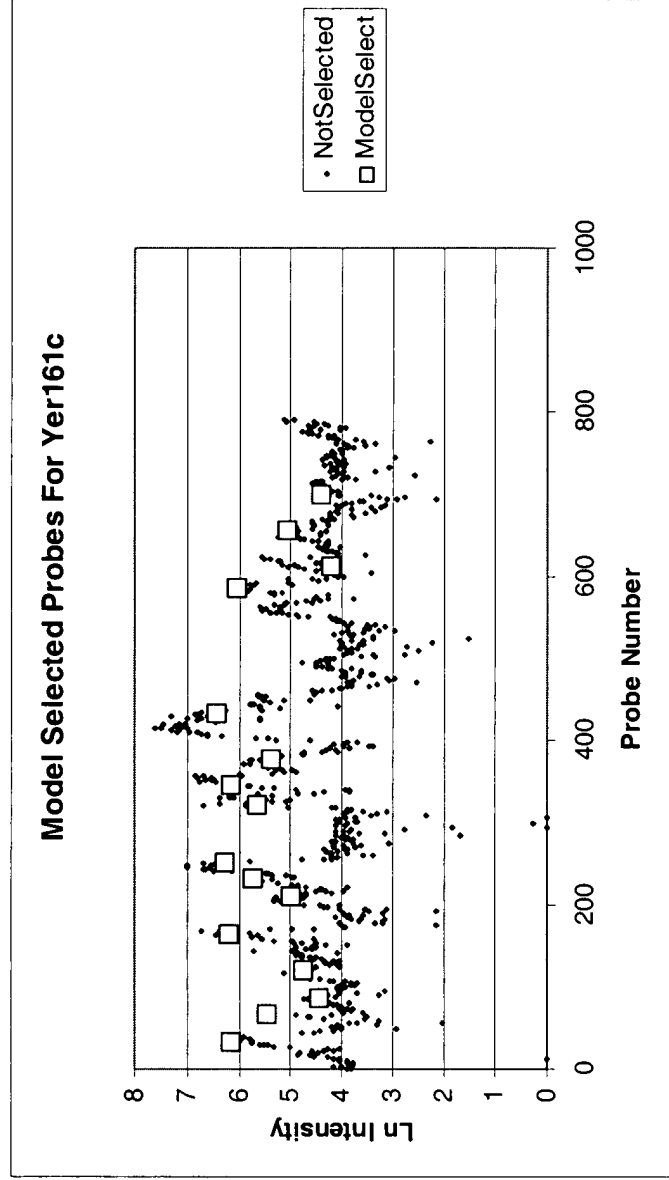


Figure 29

Comparison of AveDiff Values of all Yeast Test Chip Genes: New vs Random vs Rules Selection

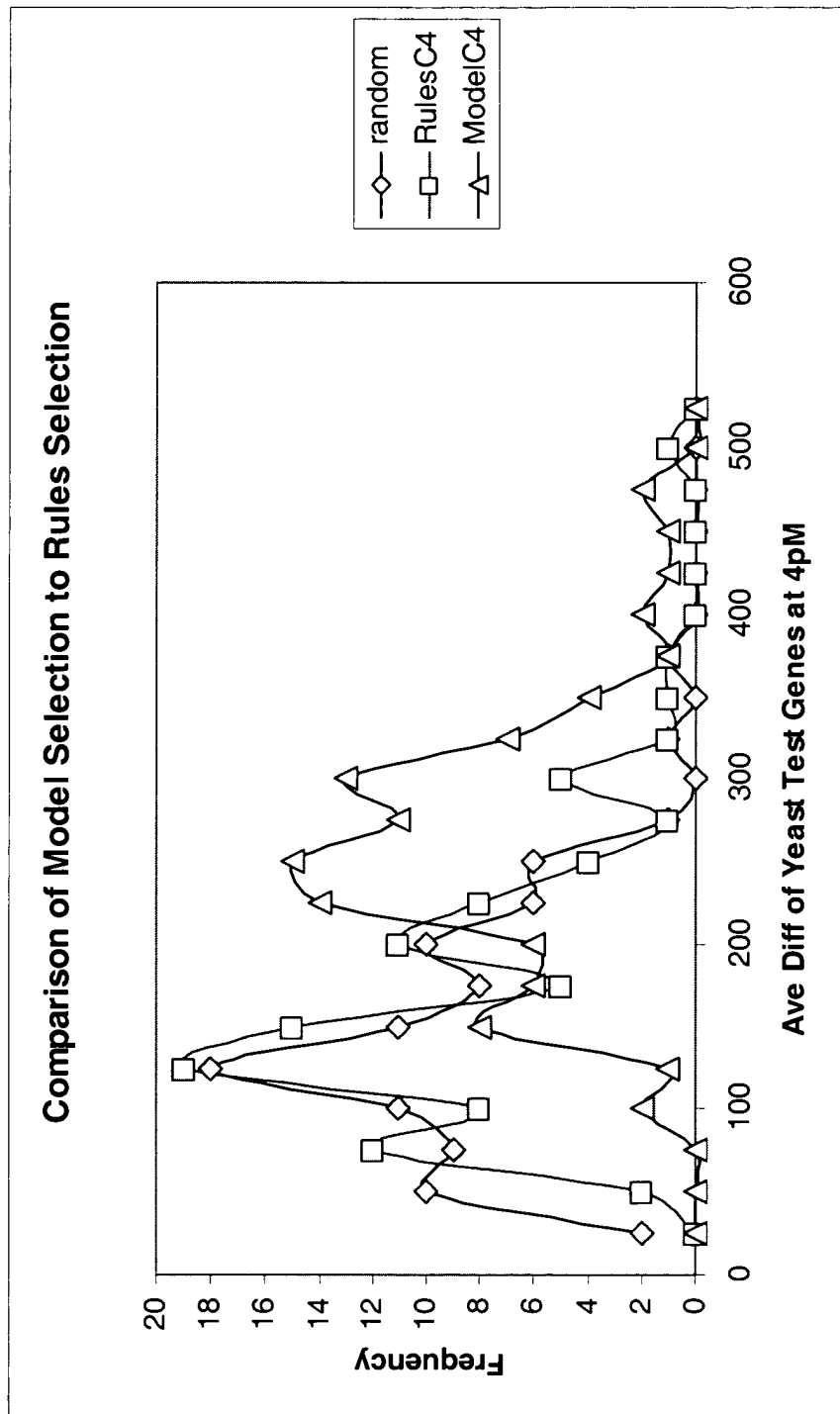


Figure 30